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Systematic analysis of liver cancer metabolism - lessons from mice and humans

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Metabolic reprogramming is a required step during oncogenesis. It is triggered by activation of oncogenes and loss of tumor suppressors and leads to an activation of central metabolic pathways to support cell growth and proliferation.

In order to quantify the usage and activity of metabolic pathways *in vitro* and *in vivo* we have developed pulsed stable isotope resolved metabolomics (pSIRM). The applied GC-MS based technology enables the absolute quantification of metabolites and at the same time the determination of stable isotope incorporation.

Using pSIRM we have characterized the action of inhibitors of glycolysis in cell cultures. We observed that the commonly used compound 2-deoxyglucose is not a specific glycolytic inhibitor, the action of 3-bromopyruvate as glycolytic inhibitor could be confirmed. We next analyzed the metabolic program of hepatocellular carcinoma using quantitative proteomics and *in vivo* isotope labelling. We further characterized the action of glycolytic inhibitors in a HCC-mouse model. Finally, we compared the metabolic phenotype of HCC between mice and humans. And observed striking similarities at the metabolic level.

Biography:

Stefan Kempa is group leader at the Berlin Institute for Medical Systems Biology BIMS at the Max Delbrück Center for Molecular Medicine in Berlin, Germany. The group established gas chromatography coupled mass spectrometry (GC-MS) as well as liquid chromatography coupled mass spectrometry (LC-MS) based techniques to monitor the metabolome and the proteome. In addition they have developed pulsed stable isotope resolved metabolomics (pSIRM) as a tool for a dynamic metabolic characterization of cellular metabolism. Using this technology they investigate cancer metabolism aiming to improve the understanding of cancer. The specific interest is to understand metabolic dependencies of cancer cells and to improve cancer treatment.